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Docket No. MNM/001 PCT

IN THE PATENT COOPERATION TREATY
INTERNATIONAL PRELIMINARY EXAMINATION AUTHORITY/US

Applicant(s) : MILLENNIUM PHARMACEUTICALS, INC., et al.

Int'l Appln. No. : PCT/US2003/032812

Filed : October 16, 2003

For : SPLEEN TYROSINE KINASE CATALYTIC DOMAIN:
CRYSTAL STRUCTURE AND BINDING POCKETS
THEREOF

New York, New York 10020
April 27, 2004

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AMENDMENT UNDER PCT ARTICLE 34

Sir:

Applicants submit herewith an Amendment Under PCT Article 34 concurrently with a Chapter II Demand Under PCT Article 31. Applicants request that the International Preliminary Examining Authority enter this Amendment.

Please amend the application as follows:

IN THE DESCRIPTION

Please replace page 16 with substitute page 16
submitted herewith in triplicate.

measured in negative values, the lower the value the more favorable the interaction.

[0001] The term "motif" refers to a group of amino acid residues in the Syk_{cat} protein or homologue that defines a structural compartment or carries out a function in the protein, for example, catalysis, structural stabilization, or phosphorylation. The motif may be conserved in sequence, structure and function.

5 The motif can be contiguous in primary sequence or three-dimensional space. Examples of a motif include but are not limited to the phosphorylation lip or activation loop, the glycine-rich phosphate anchor loop, the catalytic loop, the DFG or DFGWSxxxxxxxxRxTxCGTxDYLPP
10 loop (SEQ ID NO: 11) (see, Xie et al., *Structure*, 6 pp. 983-991 (1998); Giet and Prigent, *J. Cell. Sci.*, 112, pp. 3591-601 (1991)) and the degradation box.

15 [0002] The term "part of a binding pocket" refers to less than all of the amino acid residues that define the binding pocket. The structure coordinates of residues 20 that constitute part of a binding pocket may be specific for defining the chemical environment of the binding pocket, or useful in designing fragments of an inhibitor that may interact with those residues. For example, the portion of residues may be key residues that play a role 25 in ligand binding, or may be residues that are spatially related and define a three-dimensional compartment of the binding pocket. The residues may be contiguous or non-contiguous in primary sequence. In one embodiment, part 30 of a binding pocket has at least two amino acid residues, preferably at least four, six or eight amino acid residues.

[0003] The term "part of a Syk_{cat} protein" or "part of a Syk_{cat} homologue" refers to less than all of the amino

REMARKS

Applicants submitted a Sequence Listing on January 22, 2004. Accordingly, applicants have amended page 16 of the specification to insert the Sequence ID Number corresponding to the sequence on page 16, line 13.

No new matter has been introduced by these changes.

Applicants request that the International Preliminary Examining Authority consider the above remarks and replace page 16 of the application with substitute page 16 submitted herewith in triplicate.

Respectfully submitted,

Michele A. Kercher

James F. Haley, Jr. (Reg. No. 27,794)
Li Su (Reg. No. 45,141)
Attorneys for Applicants
Michele A. Kercher (Reg. No. 51,869)
Agent for Applicants

FISH & NEAVE
Customer No. 1473
1251 Avenue of the Americas
New York, New York 10020-1104
Tel.: (212) 596-9000
Fax: (212) 596-9090